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REMARKS

Applicant has carefully reviewed and considered the Office Action mailed on June 26, 2003, and the references cited therewith.

Claims 1-18 are now pending in this application. Claim 1 has been amended to correct an inadvertent typographical error; hence, "polypeptide" has been deleted and "polynucleotide" has been substituted therefor. Claims 1 and 12 have also been amended to include a description of the features of the present arrays. Hence, claims 1 and 12 include the following terminology: "each array comprising discrete probe features, each probe feature comprising probes, all having the same sequence, within a discrete known location within the array." Support for subject matter relating to such discrete probe features can be found throughout the specification, for example, at page 19, lines 4-8; page 29, lines 23-27; throughout the Examples; and Figures 2a-c, and 6a. Applicant submits that such amendment adds no new matter.

§103 Rejection of the Claims

Claims 1-18 were rejected under 35 USC § 103(a) as allegedly unpatentable over Cantor et al. (U.S. 5,631,134) in view of Southern (U.S. 5,700,637) and Huang et al. (U.S. 6,287,778) and/or Lipshutz et al (U.S. 6,300,063).

As a preliminary matter, Applicant submits that Huang et al. (U.S. 6,287,778, filed Oct. 19, 1999) is not prior art to the present invention because it was filed after the present application (filed Sep. 13, 1999). Applicant requests withdrawal of this rejection under 35 USC § 103(a) with respect to Huang et al. (U.S. 6,287,778).

The above rejections under 35 USC § 103(a), with respect to the other references cited, are respectfully traversed. To establish a *prima facie* case of obviousness, three basic criteria must be met. First, there must be some suggestion or motivation either in the cited references themselves or in the knowledge generally available to an art worker, to modify the reference or to combine reference teachings to as to arrive at the claimed method. Second, the art must provide a reasonable expectation of success. Finally, the prior art reference must teach or suggest all the claim limitations (M.P.E.P. § 2143). The teaching or suggestion to arrive at the claimed method and the reasonable expectation of success must both be found in the prior art, not in Applicant's disclosure (M.P.E.P. § 2143 citing with favor, *In re Vaeck*, 20 U.S.P.Q.2d 1438 (Fed. Cir. 1991)).

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Applicant submits that a *prima facie* case of obviousness cannot be established from the combination of cited references because there is no suggestion or motivation to combine the references so as to arrive at the claimed methods, there is no reasonable expectation of success that the references could produce the claimed methods and the references do not teach all the claim limitations.

One of skill in the art could not reasonably expect from the confusing and speculative teachings of Cantor et al. (U.S. Patent 5,631,134) to produce an array with a complete set of n-mers that could successfully work in the methods of the present invention. In particular, Cantor et al. provide no disclosure of an actual hybridization procedure that yields any sequence information whatsoever for a nucleic acid. For example, Cantor et al. describes a single synthesis of a single pool of 5-mers consisting of variable bases (N₅) whose sequences are unknown (Example 2). These small molecular weight 5-mers are separated from the plasmid used for their synthesis, linked to biotin and then attached to a streptavidin-coated surface. Hence, the "array" made according to Cantor et al. is simply a mixture of oligonucleotides whose sequences and locations on a solid support are unknown. Cantor et al. explicitly state:

The initial array containing about a thousand probes. The particular sequence at any location in the array will not be known.

Cantor et al. (U.S. Patent 5,631,134) col. 13, lines 14-16. According to Cantor et al., "identification of particular elements of the array" is accomplished by hybridization with known nucleic acid sequences. *Id.*, col. 13, lines 19-21. Thus, if the "array" provided by Cantor et al. has about 1000 different probes, about one thousand different hybridization reactions would therefore have to be performed in order to identify the sequence of each probe in the array. The tedium and inefficiency of such repeated hybridization procedures would in itself undermine the expectations one of skill in the art might have of successfully generating and then productively using an array having a complete set of n-mers.

Furthermore, Applicant submits that the array described by Cantor et al. could not reasonably survive intact during the 1000 or more hybridization reactions needed to establish the identity and location of each probe in a 5-mer (or larger) n-mer array. As is known to one of skill in the art, single-stranded probes are prone to nuclease digestion, and such nucleases can be present in contaminated or improperly handled reagents and as well as in samples of nucleic acids (e.g., targets used as known nucleic acids for determining the 5-mer sequences). Even if

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the skilled artisan successfully guarded against nuclease digestion, the 1000 or more cycles of heating and exposure to hybridization solutions would tend to degrade the Cantor et al. "array" and thereby undermine its utility for its intended purposes.

Hence, Cantor et al. utilizes the term "determinable" (i.e., unknown but theoretically identifiable) with reference to the probe sequences throughout U.S. Patent 5,631,134. See col. 3, lines 58-59; col. 5, line 52; col. 6, line 57; col. 8, line 6; col. 8, line 27; col. 9, line 4. Applicant submits that such "determinable" probe "arrays" that have no known sequences and no identified positions also have no practical utility for sequence analysis applications. An array cannot be used for sequencing unless the sequence and location of each probe on an array is known without a doubt. One of skill in the art could therefore receive no guidance whatsoever from the "determinable" arrays of the Cantor et al. disclosure that would lead to the already determined arrays and methods of the invention.

Moreover, even if one of skill in the art did perform one thousand different hybridization reactions, Applicant submits the separate single 5-mer probes on the Cantor et al. "array" could not be reliably identified, located or even detected by such hybridization reactions. While there may be more than one oligonucleotide of the same sequence in such an "array," Cantor et al. does not teach how to cluster the same-sequence oligonucleotides into a single location (or "feature") as provided in the present application. As is known to one of skill in the art, it is almost impossible to detect hybridization between a single nucleic acid and its complement, especially when the nucleic acid is as short as five nucleotides -- one of skill in the art simply cannot attach enough label molecules to a single complementary nucleic acid to allow reliable location of a single 5-mer probe attached to the "array" provided by Cantor et al. This may be why the only actual data provided in Cantor et al. is a graph of the ratio of radioactive counts after a "hot wash" versus a "cold wash" from a pool of probes attached to beads (Example 13, Fig. 12A). Neither the location nor sequence of the probes in an array is needed to generate the data provided by Cantor et al. in Fig. 12A.

Applicant submits that use of terms "array" and "sequencing" by Cantor et al. is misleading because Cantor et al. do not teach how to make an array with any useful features that would permit actual sequencing information to be obtained. Instead, Cantor et al. is limited to vague, confusing and hypothetical teachings that would not guide one of skill in the art to the present invention. The undetermined "arrays" described by Cantor et al. are thus not the arrays

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described and claimed by the invention. Cantor et al. simply has not disclosed how to make a useful array of probes with known sequences at known locations, let alone a complete set of n-mers. Hence, Cantor et al. (U.S. Patent 5,631,134) fails to teach the methods of the invention that involve using arrays of probe features where the sequence and location of the probes in those features are known. Similarly, Cantor et al. fails to effectively teach arrays with complete sets of n-mers. Thus, Cantor et al. not only fails to provide a reasonable expectation of success but also fails to teach or suggest all the claim limitations (M.P.E.P. § 2143).

Moreover, like the Cantor et al. reference, the Southern (U.S. 5,700,637) and Lipshutz et al (U.S. 6,300,063) references do not provide a reasonable expectation of success of generating an array having a complete set of n-mers that can successfully be used in the methods of the invention. To render an invention obvious, the combination of the cited art must teach or suggest the claimed invention and provide a reasonable expectation of success in preparing the claimed invention. *In re Vaeck*, 947 F.2d 488, 20 U.S.P.Q.2d 1438 (Fed. Cir. 1991); *In re O'Farrell*, 853 F.2d 894, 7 U.S.P.Q.2d 1673 (Fed. Cir. 1988). Applicant submits that even when combined, one of skill in the art would not have a reasonable expectation that the teachings of Cantor, Southern and Lipshutz could successfully prepare an array with a complete set of n-mers that could be used in the claimed methods for determining the presence of a mutation in a target polynucleotide, or determining whether two or more target polynucleotides are identical.

While Southern may have identified several problems relating to generating and utilizing arrays with complete sets of n-mers, Southern does not solve these problems. In particular, Southern describes "some statistics" at col. 4, lines 14-46, showing that a large number of sequence combinations are needed to analyze a sequence, but does not solve the problem of generating and using an array with a complete set of n-mers that would involve such a large number of sequence combinations. For example, in Example 1, Southern synthesizes only oligo-dT₁₀-oligo dT₁₄ on a slide. In Example 2, Southern synthesizes only the following two oligonucleotides 3' CCC GCC GCT GGA (cosL) and 3' CCC GCC TCT GGA. In Examples 3 and 4, Southern synthesizes only the oligonucleotides shown in Table 1. In Example 6, only oligonucleotides relating to the wild type and mutant (sickle cell anemia) β -globin gene were used on a slide. In Example 7, Southern prepares a slide with 256 octapurines (eight nucleotide oligonucleotides with only adenine and guanine residues). Therefore, all of these examples

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generate discrete sets of oligonucleotides and do not come even close to generating a complete set of n-mers.

Furthermore, the array fabrication techniques disclosed in Southern is not amenable to making an n-mer array suitable for the presently claimed invention. The Southern arrays are fabricated by separating features with rubber tubing. The tubes are glued to a glass plate at 8-mm intervals (see Example 3, col. 10, lines 15-28). The glass plate itself was 220 x 220 mm in size and allowed for a total of 78 different oligonucleotides (Table 1). As described by Southern at col. 5, lines 5-22, when large genomes are analyzed the area required to manufacture arrays with a suitable number of features using the Southern techniques becomes prohibitory (e.g. 2500 pieces of film for the human genome). Clearly, Southern has not developed the technology needed for generating arrays with complete sets of n-mers.

Thus, Southern (U.S. 5,700,637) is limited to hypothetical discussions relating to an "Apparatus and Method for Analyzing Polynucleotide Sequences and Method of Generating Oligonucleotide Arrays." Aside from the fact that the methods and arrays described by Southern are purely theoretical and Southern provides no teaching on how to actually generate a usable array comprising a complete set of n-mer probes, how to actually perform a hybridization reaction that would actually distinguish single base mismatches and how to discriminate such single base mismatches from noise and non-mismatches once such a hybridization reaction has been performed, Southern does not disclose all elements of the present invention. For example, Southern does not disclose that each probe comprises a double stranded region and a single-stranded n-mer overhang region (see e.g., col. 7, lines 2-9; col. 8, line 59 to col. 9, line 35; and Examples 1-2, describing synthesis and use of a single-stranded oligonucleotide on CPG or glass supports). Moreover, Southern does not disclose or teach hybridizing the target or reference polynucleotide to probes having such double stranded and single-stranded overhangs. Such a distinction may be useful in some embodiments of the present invention because, as described in the present specification at page 17, lines 17-18, the double-stranded region allows a ligation step to be performed after the hybridization step in the method. Ligation allows thorough washing of the array to remove non-hybridized polynucleotide fragments (specification at page 22, lines 7-8). Thus, Southern does not teach or disclose every element of the invention.

Lipshutz et al (U.S. 6,300,063) is directed to detection of polymorphisms in particular selected genes, not to the presently claimed methods that use arrays having complete sets of n-

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mers. Hence, the arrays contemplated by Lipshutz are designed as customized arrays for detecting polymorphisms in only certain target genes (not all genes). For example, in the Abstract, Lipshutz states that the disclosed methods "employ arrays of oligonucleotide probes that are complementary to target nucleic acids which correspond to the marker sequences of an individual." In the Summary of the invention, Lipshutz states that the arrays employed comprise "at least one detection block of probes, said detection block including a first group of probes that are complementary to said target nucleic acid sequence." Lipshutz et al (U.S. Patent 6,300,063), col. 2, lines 19-22. In the Detailed Description of the Invention, Lipshutz describes procedures for identifying specific polymorphisms so that arrays can be developed to detect those specific polymorphisms. For example, Lipshutz teaches that genomic sequencing of genomic material from large numbers of individuals, ligation methods and restriction patterns can be used to identify known polymorphisms. Applicant submits that if Lipshutz intended that the array have a complete set of n-mers, such focus on pre-defining the polymorphism would not be needed. Hence, the arrays described by Lipshutz do not teach or suggest the claimed invention.

Moreover, Applicant submits that there is no motivation to combine the teachings of Cantor with the teachings of Southern and Lipshutz. One would not have been motivated to combine Cantor's undetermined arrays with Southern's single-stranded probes and Lipshutz's customized arrays to produce the presently claimed invention, particularly since, as discussed above, none of these references effectively teach the use of complete n-mer arrays to conduct the methods of the invention.

It is respectfully submitted that the Examiner is employing hindsight to arrive at Applicant's invention in the absence of any suggestion in the cited art to take Applicant's approach. The Examiner is reminded that it is impermissible to use Applicant's specification as a template to arrive at the conclusion that the claimed invention is obvious. *In re Fritsch*, 23 U.S.P.Q.2d 1780, 1782 (Fed. Cir. 1992). For example, it is improper to presume that Cantor et al. or Southern has the features or arrays described and claimed by the present invention when the evidence suggests otherwise. Similarly, it would be improper to presume that Lipshutz discloses a complete set of n-mers when the teachings of Lipshutz are clearly directed to detecting polymorphism in certain genes. Thus, it is improper, in determining whether a person of ordinary skill would have been led to the invention by this combination of references, simply

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to use that which the inventor taught against its teacher. *In re Lee*, 61 USPQ2d, 1430, 1434 (Fed. Cir. 2002).

Applicant submits that without hindsight at the time of the invention, no reasonable likelihood existed of combining Cantor et al. (U.S. 5,631,134), Southern (U.S. 5,700,637) and Lipshutz et al (U.S. 6,300,063) to produce the invention of the rejected claims. (See MPEP 2143.02 which mandates a reasonable likelihood of success in making the combination.) Cantor et al. and Southern fail to produce an array with a complete set of n-mers and provide only speculation as to how one might produce arrays with such large numbers of oligonucleotide probes. Cantor lacks the features of the invention and Southern fails to disclose probes that are both double-stranded and single-stranded. Lipshutz is explicitly limited to use of customized arrays having less than a complete set of n-mers for detected selected polymorphisms. Hence, the combination of Cantor et al. (U.S. 5,631,134), Southern (U.S. 5,700,637) and Lipshutz et al (U.S. 6,300,063) does not produce the claimed invention. Applicant requests withdrawal of this rejection under 35 USC § 103(a) of claims 1-18.

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CONCLUSION

Applicant respectfully submits that the claims are in condition for allowance and notification to that effect is earnestly requested. The Examiner is invited to telephone Applicant's attorney (516) 795-6820 to facilitate prosecution of this application.

If necessary, please charge any additional fees or credit overpayment to Deposit Account No. 19-0743.

Respectfully submitted,

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The undersigned hereby certifies that this correspondence is transmitted by facsimile (FAX NO. 703-308-8724) to: Attn.: Examiner Betty J. Forman, GAU 1634, Commissioner of Patents, P. O. Box 1450, Alexandria, VA 22313-1450, on this 26 day of August, 2003.

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